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Figure 1

Cloning of the endothelial cell tropic and leukotropic clinical isolate VR1814 as FIX-BAC

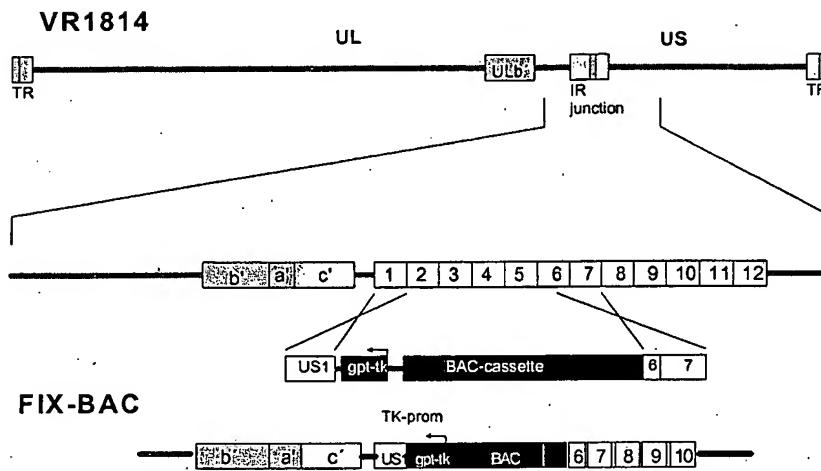


Fig. 1 Construction of FIX-BAC. A gpt-tk-BAC cassette was introduced into the US2-6 region of the parental virus VR1814 as described in patent application PCT/EP02/01867 (WO 02/066629).

Figure 2

RVFIX virus mutants

RVFIX Δ ULb
RVFIX Δ UL132-128
RVFIX Δ UL133-148
RVFIX Δ UL132-130
RVFIX Δ UL131K
RVFIX Δ UL130
RVFIX Δ UL128K
RVFIX Δ UL132K
RVFIX Δ UL148
RVFIX Δ UL146-147
RVFIX Δ UL127

Deletion according to (Chee, Bankier et al., 1990)

nt 175662-189347
nt 174857-176865
nt 177896-189347
nt 175662-177743
nt 176377-176776
nt 175662-176314
nt 174953-175387
nt 177076-177752
nt 177896-178644
nt 179069-179966
nt 174467-174770

Fig. 2 List of RVFIX virus mutants and determination of the mutation (kanamycin cassette insertion) according to annotation by {Chee, Bankier, et al. 1990 269 /id}

Figure 3 shows an agarose gel and Southern Blot of RVFIX and RVFIX mutant viruses.

Figure 3

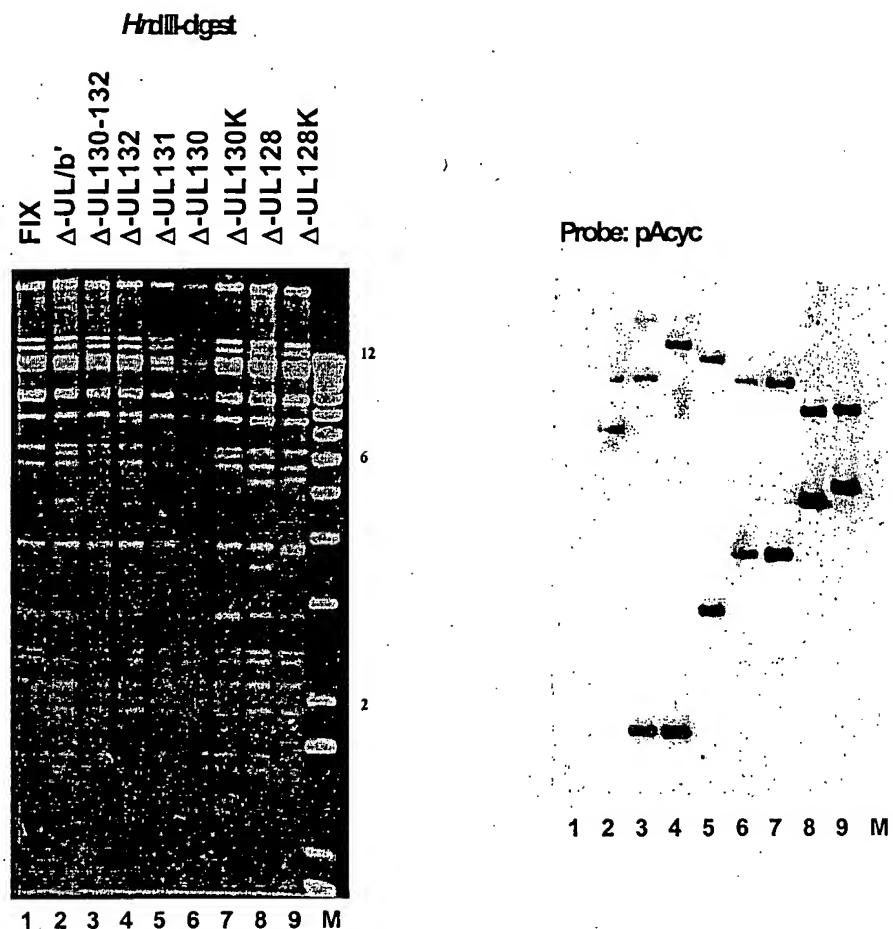


Fig.3 DNA derived from individually grown FIX-BAC clones (lane 1) or FIX-BAC mutant clones ΔULb', ΔUL130-132, ΔUL132, ΔUL131, ΔUL130, ΔUL130K, ΔUL128 and ΔUL128K (lanes 2-9) was digested with *Hind*III and run on a 0.5% agarose gel.

Figure 4

A

FIX 176834-GTCTGCAACATGCCGGCTGTCTGGCTGTCCTGTTGTCTGTGCGCCGTGGTGTG
 RACE_95_3 GTCTGCAACATGCCGGCTGTCTGGCTGTCCTGTTGTCTGTGCGCCGTGGTGTG
 RACE_95_8 GTCTGCAACATGCCGGCTGTCTGGCTGTCCTGTTGTCTGTGCGCCGTGGTGTG
 RACE_95_11 GTCTGCAACATGCCGGCTGTCTGGCTGTCCTGTTGTCTGTGCGCCGTGGTGTG

FIX GGTCACTGCCAGCGGGAGACCGCAGAAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_3 GGTCACTGCCAGCGGGAGACCGCAGAAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_8 GGTCACTGCCAGCGGGAGACCGCAGAAAAAA--CGATTATTACCGAGTACCGCATTACT
 RACE_95_11 GGTCACTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACT

FIX GGGACCGCTGCTCTCGCGCCTGCCTGACCAAACCCCTAACAGTATGTGAACAGCTCG
 RACE_95_3 GGGACCGCTGCTCTCGCGCCTGCCTGACCAAACCCCTAACAGTATGTGAACAGCTCG
 RACE_95_8 GGGACCGCTGCTCTCGCGCCTGCCTGACCAAACCCCTAACAGTATGTGAACAGCTCG
 RACE_95_11 GGGACCGCTGCTCTCGCGCCTGCCTGACCAAACCCCTAACAGTATGTGAACAGCTCG

FIX TGGACCTCACGTTGAACCTACCAACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTG
 RACE_95_3 TGGACCTCACGTTGAACCTACCAACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTG
 RACE_95_8 TGGACCTCACGTTGAACCTACCAACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTG
 RACE_95_11 TGGACCTCACGTTGAACCTACCAACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTG

FIX TCAAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAAGGGCGAACGGGT
 RACE_95_3 TCAAGAG-----
 RACE_95_8 TCAAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAAGGGCGAACGGGT
 RACE_95_11 TCAAGAG-----

FIX AACGGGTAGGTAAACCGCATGGGTGTGAAATGACGTTCGAACCTGTGCTTGCAAGAATCA
 RACE_95_3 -----
 RACE_95_8 AACGGGTAGGTAAACCGCATGGGTGTGAAATGACGTTCGAACCTGTGCTTGCAAGAATCA
 RACE_95_11 -----

FIX ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCG
 RACE_95_3 ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCG
 RACE_95_8 ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCG
 RACE_95_11 ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGGCG

FIX CCAACAAAAGGACCACGTTCAACGCCCGGTTCGCTGGCGCTCACGCCCGAACCTCG
 RACE_95_3 CCAACAAAAGGACCACGTTCAACGCCCGGTTCGCTGGCGCTCACGCCCGAACCTCG
 RACE_95_8 CCAACAAAAGGACCACGTTCAACGCCCGGTTCGCTGGCGCTCACGCCCGAACCTCG
 RACE_95_11 CCAACAAAAGGACCACGTTCAACGCCCGGTTCGCTGGCGCTCACGCCCGAACCTCG

FIX AGTTCAAGCGTGCCTTGCCTGCAACTAGCCTGCGTCA-176346
 RACE_95_3 AGTTCAAGCGTGCCTTGCCTGCAACTAGCCTGCGTCA
 RACE_95_8 AGTTCAAGCGTGCCTTGCCTGCAACTAGCCTGCGTCA
 RACE_95_11 AGTTCAAGCGTGCCTTGCCTGCAACTAGCCTGCGTCA

B

FIX 175631-CCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_3 CCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_8 CCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
 RACE_95_13 CCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG

FIX7 GGTACAGCCCGTGCCTGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCAAC
 RACE_95_3 GGTACAGCCCGTGCCTGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCAAC
 RACE_95_8 GGTACAGCCCGTGCCTGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCAAC
 RACE_95_11 GGTACAGCCCGTGCCTGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCAAC

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

CACCCGCCGGAACGCTGTTACGATTTCAAAATGTCAATCGCTTCACCGTGC~~G~~TACGTA
 CACCCGCCGGAACGCTGTTACGATTTCAAAATGTCAATCGCTTCACCGTGC~~G~~TACGTA
 CACCCGCCGGAACGCTGTTACGATTTCAAAATGTCAATCGCTTCACCGTGC~~G~~TACGTA
 CACCCGCCGGAACGCTGTTACGATTTCAAAATGTCAATCGCTTCACCGTGC-----

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

TTTTTATGATTGCTGCGTTCTGTGGTGC~~G~~TCTGGATTTGTCTCTCGACGTTCTGATAG
 TTTTCATGATTGCTGCGTTCTGTGGTGC~~G~~TCTGGATCTGTCTCTCGACGTTCTGATAG
 TTTTCATGATTGCTGCGTTCTGTGGTGC~~G~~TCTGGATCTGTCTCTCGACGTTCTGATAG

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

CCATGTTCCATCGACGATCCTCGGGAA~~T~~GCCAGAGTAGATTTCATGAATCCAC~~A~~GGCTG
 CCATGTTCCATCGACGATCCTCGGGAA~~T~~GCCAGAGTAGATTTCATGAATCCAC~~A~~GGCTG
 CCATGTTCCATCGACGATCCTCGGGAA~~T~~GCCAGAGTAGATTTCATGAATCCAC~~A~~GGCTG
 -----GCTG

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCC~~G~~GAGAAAACGGCTGAGATT~~C~~GGGGATC
 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCC~~G~~GAGAAAACGGCTGAGATT~~C~~GGGGATC
 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCC~~G~~GAGAAAACGGCTGAGATT~~C~~GGGGATC
 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCC~~G~~GAGAAAACGGCTGAGATT~~C~~GGGGATC

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

GTCACCACCATGACCCATT~~C~~ATTGACACGCCAGGT~~C~~GTACACAACAAACTGACGAGCTGC
 GTCACCACCATGACCCATT~~C~~ATTGACACGCCAGGT~~C~~GTACACAACAAACTGACGAGCTGC
 GTCACCACCATGACCCATT~~C~~ATTGACACGCCAGGT~~C~~GTACACAACAAACTGACGAGCTGC
 GTCACCACCATGACCCATT~~C~~ATTGACACGCCAGGT~~C~~GTACACAACAAACTGACGAGCTGC

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

AACTACAATCC~~G~~TAAGTCTCTCCTCGAGGGC~~T~~TAACGCC~~T~~ATGGGAAAGTAAGACAGA
 AACTACAATCC-----
 AACTACAATCC-----
 AACTACAATCC-----

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

GGGACAAAACATCATTAAAAAAAGTCTAATT~~C~~ACGTTTG~~T~~ACCCCCCCT~~T~~CCCCTC

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

CGTGTGT~~A~~GGTTATACCTCGAACGCTGACGGCGAATACGCTGCGCAA~~A~~GTGAACGACA
 -----GTTATACCTCGAACGCTGACGGCGAATACGCTGCGCAA~~A~~GTGAACGACA
 -----GTTATACCTCGAACGCTGACGGCGAATACGCTGCGCAA~~A~~GTGAACGACA
 -----GTTATACCTCGAACGCTGACGGCGAATACGCTGCGCAA~~A~~GTGAACGACA

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

AGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAAT
 AGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAAT
 AGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAAT
 AGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAAT

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

ACGACAAGATAACCCGGATCGTGGGC~~T~~GGATCAGTACCTGGAGAGCGTTAAGAAACACA
 ACGACAAGATAACCCGGATCGTGGGC~~T~~GGATCAGTACCTGGAGAGCGTTAAGAAACACA
 ACGACAAGATAACCCGGATCGTGGGC~~T~~GGATCAGTACCTGGAGAGCGTTAAGAAACACA
 ACGACAAGATAACCCGGATCGTGGGC~~T~~GGATCAGTACCTGGAGAGCGTTAAGAAATACA

FIX
 RACE_95_3
 RACE_95_8
 RACE_95_11

AACGGCTGGATGTGTG~~C~~CCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA-174887
 AACGGCTGGATGTGTG~~C~~CCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA---
 AACGGCTGGATGTGTG~~C~~CCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA---
 AACGGCTGGATGTGTG~~C~~CCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA---

C

FIX 174892-CGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGGTGTGTTGTCCGA-174841

RACE_95_3 -- CGCTAAAATGGGCTATATGCTGCAGTGAATA**AATAAA**ATGTGTGTTGTCCGCAAAAAAAA --
RACE_95_8 -- CGCTAAAATGGGCTATATGCTGCAGT A**ATAA**TAAAATGTGTGTTGTCCAAAAAAA --
RACE_95_11 -- CGCTAAAATGGGCTATATGCTGCAGTGAATA**AATAAA**ATGTGTGTTGTCCAAAAAAA --

Fig. 4 UL131-128 mRNA processing – Panels (A-C) compare FIX-BAC DNA sequence (numbered according to Chee et al.) to a set of cDNA sequences from RACE clones 95-3, 95-8 and 95-11 (A) UL131 region, (B) UL128 region, (C) UL131-128 transcripts 3' end. Start codons, stop codons and the polyA site are in bold face, mRNA processing signals (splice donor sequence, splice acceptor sequence, AATAAA signal) are grey-shaded.

Figure 5

Fig. 5 Exon-intron organization of the FIX-BAC UL131-128 genetic locus. UL131 (green); UL130 (orange); UL128 (blue); UL128x1 C-terminus (light blue).

Figure 6

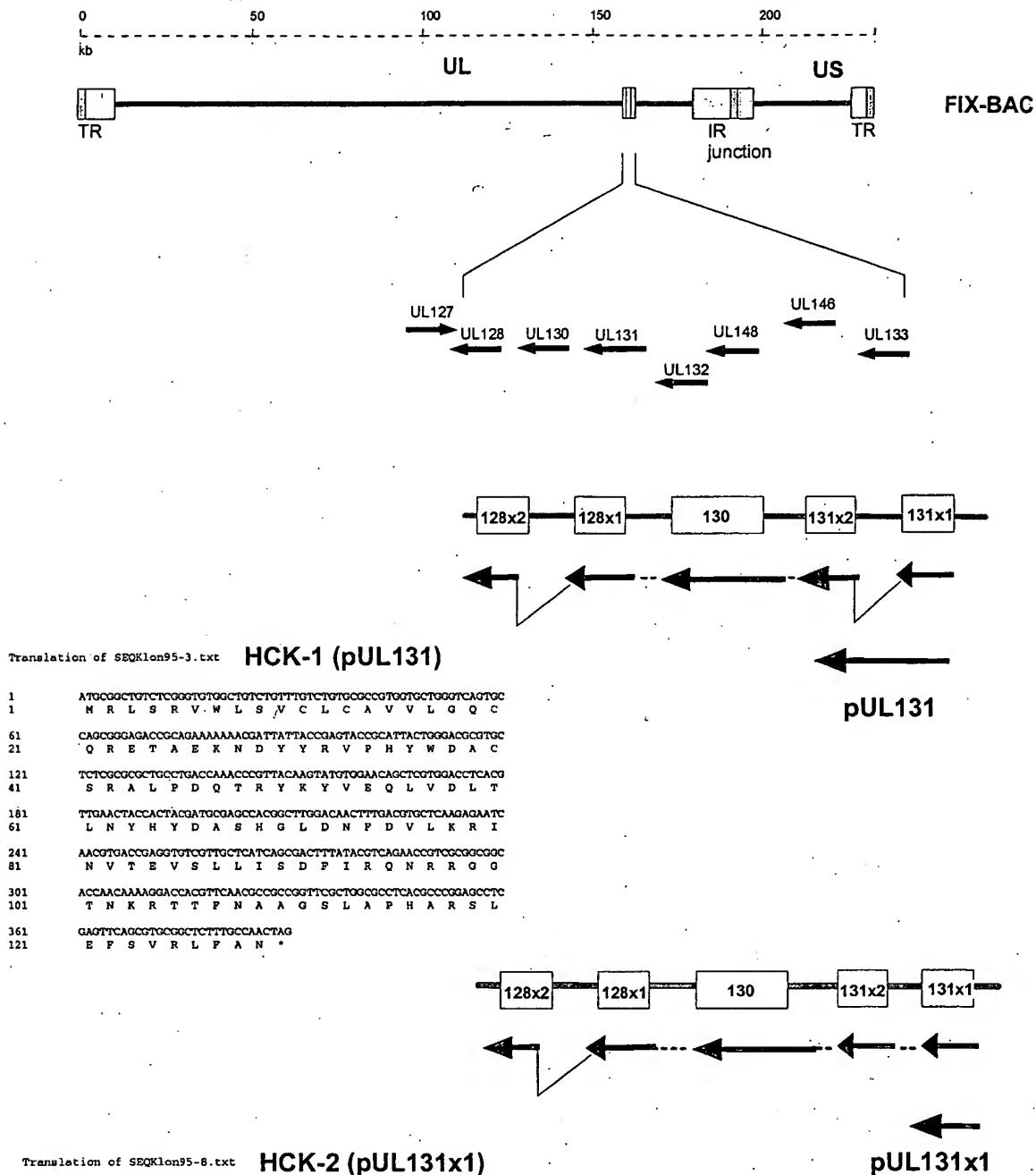
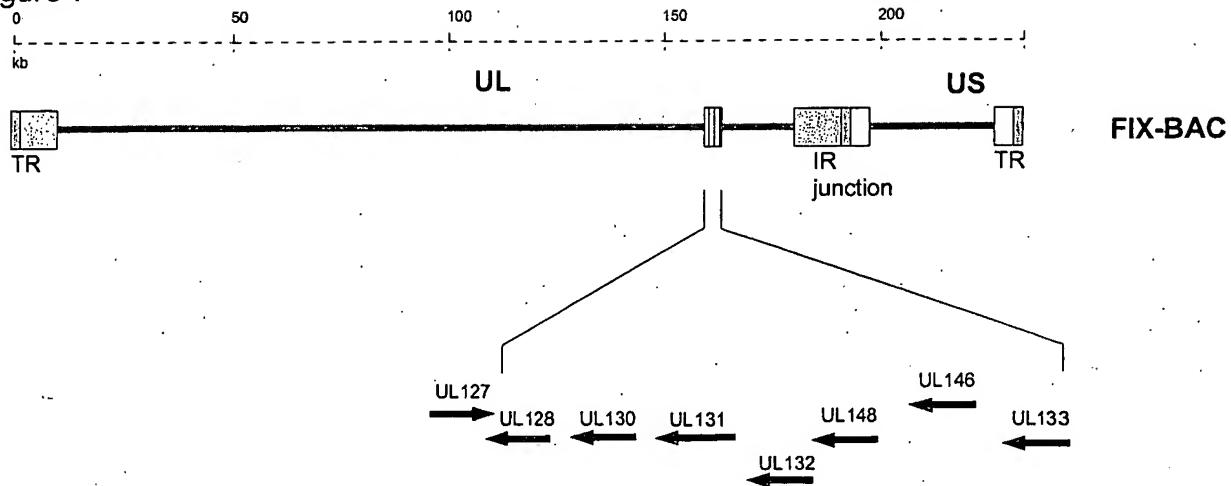


Fig. 6 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel RACE clone 95-3 and predicted open reading frame (orf) pUL131 (HCK-1). Lower panel RACE clone 95-8 and predicted orf UL131x1 (HCK-2).

Figure 7

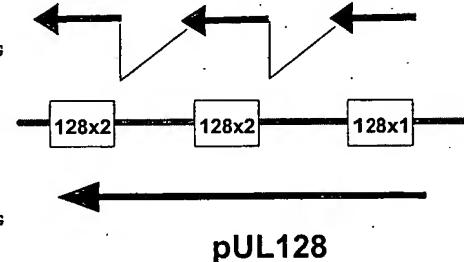


Translation of SEQ128.txt(1-563 : HCK-4 (pUL128)

```

1      ATGAGTCCAAAAACCTGACGCCCTCTTGACGGCGTTGGCTGCTATGGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGGGTACCGCAGAAGAATGTTGCAATTATAACGTCACCCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTTACGATTGAAATGTCGAATCGCTTCACCGTCGACTGCGGTGTCGGAC
41     E R C Y D F K M C N R F T V A L R C P D
181    GGCAGAAGTCTGCTACAGTCCCAGAAAACGGCTGAGATTGCGGGATCGTCACCCACATG
61     G E V C Y S P E K T A E I R G I V T T M
241    ACCCATTTCATTGACACGCCAGGTGCTACACAACAAACTGACGAGCTGCAACTACAATCTG
81     T H S L T R Q V V H N K L T S C N Y N L
301    TTATACCTCGAAGCTGACGGGCAATACGCTCGGCAAAGTGAAACGACAAGGCGCAGTAC
101    L Y L E A D G R I R C G K V N D K A Q Y
361    CTGCTGGCGCCGCTGGCAGCGTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
121    L L G A A G S V P Y R W I N L E Y D K I
421    ACCCGGATCGTGGGCCCTGGATCAGTACCTGGAGACGGCTTAAGAACACAAACGGCTGGAT
141    T R I V G L D Q Y L E S V K K H K R L D
481    GTGTGCCGCGCTAAAATGGGCTATATGCTGCACTGA
161    V C R A K M G Y M L Q *

```



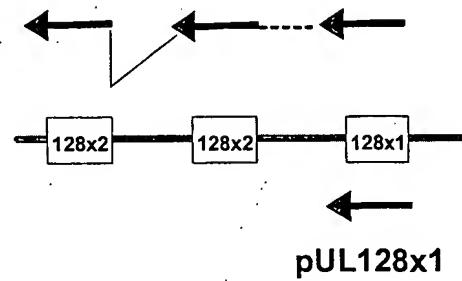
pUL128

Translation of SEQ128 x 1.txt HCK-3 (pUL128x1)

```

1      ATGAGTCCAAAAACCTGACGCCCTCTTGACGGCGTTGGCTGCTATGGGTACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGGGTACCGCAGAAGAATGTTGCAATTATAACGTCACCCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTTACGATTGAAATGTCGAATCGCTTCACCGTCGCGTACGTATTTCATGA
41     E R C Y D F K M C N R F T V A Y V F S *

```



pUL128x1

10

Fig. 7 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel SEQUL128B and predicted open reading frame (orf) pUL128 (HCK-4). Lower panel SEQUL128A and predicted orf UL128x1 (HCK-3).

Figure 8

Northern Blot Analyses

RVFIX, RVFIX mutants and laboratory strains:

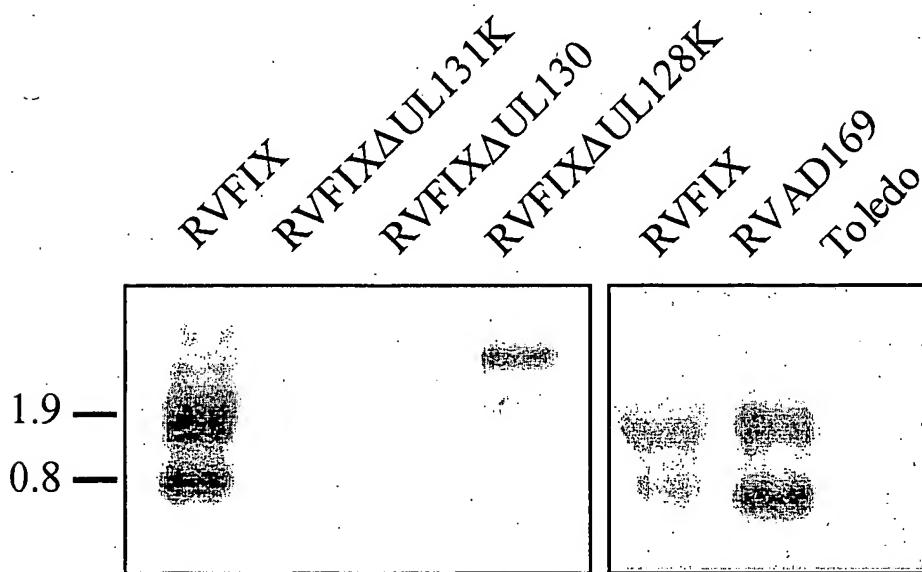


Fig. 8 mRNA was prepared from RVFIX-infected fibroblasts 4 days p.i. using Rneasy Mini, QIAshredder and Oligotex mRNA Mini kits according to the manufacturer's guidance (Qiagen). For Northern blotting, 1 μ g RNA was electrophoresed on an agarose gel according to the MOPS-formaldehyde protocol and blotted onto Hybond N+ membranes (Amersham Pharmacia). Blots were hybridized with a UL131-128 specific probe.

Figure 9

Comparison RACE clone 95-3 – FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977

Lower line: SEQKlon95-3.txt, from 1 to 1741

SEQFIX UL131-128.txt:SEQKlon95-3.txt identity= 99.66%(1735/1741)
gap=11.94%(236/1977)

1 GTCTGCAACATCGGGCTGTCTGGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGTG
1, ATGCGGCTGTCTGGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGTG
61 GGTCACTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
52 GGTCACTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
121 GACCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTACAAGTATGTGGAACAGCTCGTG
112 GACCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTACAAGTATGTGGAACAGCTCGTG
181 GACCTCACGTTGAACCTACCACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGCTC
172 GACCTCACGTTGAACCTACCACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGCTC
241 AAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCAACGGTAA
232 AAGAG.....
301 CGGGTAGGTAACCGCATGGGTGTGAAATGACGTTCGAACCTGTGCTTCAGAAC
235 AATCAAC
361 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTACGTCAGAACCGTCGGCGGCACC
244 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTACGTCAGAACCGTCGGCGGCACC
421 AACAAAAGGACCACGTTCAACGCCGCCGGTCGCTGGCGCTCACGCCGGAGCCTCGAG
304 AACAAAAGGACCACGTTCAACGCCGCCGGTCGCTGGCGCTCACGCCGGAGCCTCGAG
481 TTCAAGCGTGGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCTTC
364 TTCAAGCGTGGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCTTC
541 TGCTTCGTCACCACTTTCACTGCCGCTTGTGCGCGGTTGGCAACGCCCTGTCTGG
424 TGCTTCGTCACCACTTTCACTGCCGCTTGTGCGCGGTTGGCAACGCCCTGTCTGG
601 CGTCTCCGTGGTCAGCCTAACGGCGAACCGAGAACCGTCCCCGCCATGGCTAACTGA

484 CGTCTCCGTGGTCACGCTAACGGCGAACAGAAATCCGTCCCCGCCATGGCTAAACTGA
 661 CGTATCCCAAACCGCATGACGCCGCACGTTTACTGTCTTCTCTATCCCTCGCCCC
 544 CGTATCCCAAACCGCATGACGCCGCACGTTTACTGTCTTCTCTATCCCTCGCCCC
 721 CACGGTCCCCCTCGCAATTCCCGGGTTCCAGCGGTATCAACGGTCCCAGTGTGCA
 604 CACGGTCCCCCTCGCAATTCCCGGGTTCCAGCGGTATCAACGGTCCCAGTGTGCA
 781 ACGAGACCTGTATCTGCTGTACAACCAGGAAGGCCAGACCTGGTGGAGAGAAGCTCCA
 664 ACGAGACCTGTATCTGCTGTACAACCAGGAAGGCCAGACCTGGTGGAGAGAAGCTCCA
 841 CCTGGGTGAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACGGA
 724 CCTGGGTGAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACGGA
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGCCA
 784 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGCCA
 961 AGATTTTGGAGCGCACATGGTGCCAAGCAGACCAAGCTGCTACGTTCGTCGTCAACG
 844 AGATTTTGGAGCGCACATGGTGCCAAGCAGACCAAGCTGCTACGTTCGTCGCCAACG
 1021 ATGGCACACGTTATCAGATGTGTGATGAAACTGGAGAGCTGGCCACGTCTTCCGGG
 904 ATGGCACACGTTATCAGATGTGTGATGAAACTGGAGAGCTGGCCACGTCTTCCGGG
 1081 ACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGGAGGCCATAACCAAGACTTACA
 964 ACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGGAGGCCATAACCAAGACTTACA
 1141 CCTCTGCACCCATCCAATCTCATGTTGAGCCCGTCGCGCGCAGGGAAATTGAA
 1024 CCTCTGCACCCATCCAATCTCATGTTGAGCCCGTCGCGCGCAGGGAAATTGAA
 1201 AACCGCGCGTCATGAGTCCAAAAACCTGACGCCGTCTTGACGGCGTTGGCTGCTAT
 1084 AACCGTGCCTCATGAGTCCAAAAACCTGACGCCGTCTTGACGGCGTTGGCTGCTAT
 1261 TGGGTACAGCCCGTGCCTCGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCA
 1144 TGGGTACAGCCCGTGCCTCGGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCA
 1321 ACCACCCGCCGGAACGCTGTTACGATTCAAAATGTGCAATCGCTCACCGTCGCGTACG
 1204 ACCACCCGCCGGAACGCTGTTACGATTCAAAATGTGCAATCGCTCACCGTCGCGTACG
 1381 TATTTTCATGATTGCTGCGTTCTGTGGTGCCTCTGGATTGCTCTCGACGTTCTGAT
 1264 TATTTTCATGATTGCTGCGTTCTGTGGTGCCTCTGGATCTGCTCTCGACGTTCTGAT
 1441 AGCCATGTTCCATCGACGATCCTCGGAATGCCAGAGTAGATTTCATGAATCCACAGGC
 1324 AGCCATGTTCCATCGACGATCCTCGGAATGCCAGAGTAGATTTCATGAATCCACAGGC

1501 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCGAGAAAACGGCTGAGATTGCGGGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1384 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCGAGAAAACGGCTGAGATTGCGGGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1561 TCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1444 TCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAACCT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1621 GCAACTACAATCCGTAAAGTCTCTCCTCGAGGGCCTTACAGCCTATGGAAAGTAAGACA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1504 GCAACTACAATCC.....
1681 GAGGGACAAAACATCATTAAAAAAAAGTCTAATTACGTTTGACCCCCCTTCCCC
1517 ..
1741 TCCGTGTTGTTAGGTTATAACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAACGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1517GTTATAACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAACGA
1801 CAAGGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1565 CAAGGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGG
1861 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1625 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
1921 CAAACGGCTGGATGTGCGCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1685 CAAACGGCTGGATGTGCGCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA

Translation of SEQKlon95-3.txt: HCK-1 (pUL131)

1 ATGCGGCTGTCTCGGGTGTGGCTGTCCTGTTGTCTGTGCACCGTGGCAGGGTCAGTC
1 M R L S R V W L S V C L C A V V L G Q C

61 CAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGGGACCGCGTGC
21 Q R E T A E K N D Y Y R V P H Y W D A C

121 TCTCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG
41 S R A L P D Q T R Y K Y V E Q L V D L T

181 TTGAACTACCACTACGATGCGAGCCACGGCTTGGAACACTTGACGTGCTCAAGAGAATC
61 L N Y H Y D A S H G L D N F D V L K R I

241 AACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAAGACCGTCGCGGCCGC
81 N V T E V S L L I S D F I R Q N R R G G

301 ACCAACAAAAGGACCACGTTCAACGCCGCCGGTCGCTGGCGCCTCACGCCGGAGCCTC
101 T N K R T T F N A A G S L A P H A R S L

361 GAGTTCAGCGTGCAGCTCTTGCCAACTAG
121 E F S V R L F A N *

Figure 10**Comparison RACE clone 95-8 -FIX genomic sequence****Upper line: SEQFIX UL131-128.txt, from 10 to 1977****Lower line: SEQKlon95-8.txt, from 1 to 1849**

SEQFIX UL131-128.txt:SEQKlon95-8.txt identity= 99.78% (1845/1849)
 gap=6.47% (128/1977)

```

1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGTG
1      |||||.....ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTGTG
61     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
61     |||||.....GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
52     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
121    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCGT
121    |||||.....GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCGT
112    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCGT
181    GACCTCACGTTGAACCTACCACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGCTC
181    |||||.....GACCTCACGTTGAACCTACCACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGCTC
172    GACCTCACGTTGAACCTACCACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGCTC
241    AAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGTAA
241    |||||.....AAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGTAA
232    AAGAGGTGAGGGTACCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGTAA
301    CGGGTAGGTAACCGCATGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAAC
301    |||||.....CGGGTAGGTAACCGCATGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAAC
292    CGGGTAGGTAACCGCATGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAAC
361    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTAGACGTCAGAACCGTCGCGCGGCACC
361    |||||.....GTGACCGAGGTGTCGTTGCTCATCAGCGACTTAGACGTCAGAACCGTCGCGCGGCACC
352    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTAGACGTCAGAACCGTCGCGCGGCACC
421    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG
421    |||||.....AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG
412    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG
481    TTCAAGCGTGCGGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCTTC
481    |||||.....TTCAGCGTGCGGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCTTC
472    TTCAGCGTGCGGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCTTC
541    TGCTTCGTCACCACTTTCACTGCCTGCTCTGTGCGCGTTGGCAACGCCCTGTCTGG
541    |||||.....TGCTTCGTCACCACTTTCACTGCCTGCTCTGTGCGCGTTGGCAACGCCCTGTCTGG
532    TGCTTCGTCACCACTTTCACTGCCTGCTCTGTGCGCGTTGGCAACGCCCTGTCTGG

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601 CGTCTCCGTGGTCACGCTAACGGCGAACAGAAATCCGCCCGCCATGGCTAAACTGA
 |||||
 592 CGTCTCCGTGGTCACGCTAACGGCGAACAGAAATCCGCCCGCCATGGCTAAACTGA
 |||||
 661 CGTATCCCAAACCGCATGACGCGGCACGTTTACTGTCTTCTATCCCTGCC
 |||||
 652 CGTATCCCAAACCGCATGACGCGGCACGTTTACTGTCTTCTATCCCTGCC
 |||||
 721 CACGGTCCCCCTCGCAATTCCCAGGGTCCAGCGGGTATCAACGGTCCGAGTGTGCA
 |||||
 712 CACGGTCCCCCTCGCAATTCCCAGGGTCCAGCGGGTATCAACGGTCCGAGTGTGCA
 |||||
 781 ACGAGACCCCTGTATCTGCTGTACAACCAGGGAAAGGCCAGACCTGGTGGAGAGAAGCTCCA
 |||||
 772 ACGAGACCCCTGTATCTGCTGTACAACCAGGGAAAGGCCAGACCTGGTGGAGAGAAGCTCCA
 |||||
 841 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACGG
 |||||
 832 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACGG
 |||||
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGCC
 |||||
 892 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGCC
 |||||
 961 AGATTTTGGAGCGCACATGGTGCCAAGCAGACCAAGCTGCTACGTTCGTCGTCAACG
 |||||
 952 AGATTTTGGAGCGCACATGGTGCCAAGCAGACCAAGCTGCTACGTTCGTCGTCAACG
 |||||
 1021 ATGGCACACGTTATCAGATGTGTGATGAAACTGGAGAGCTGGGCCACGTCTCC
 |||||
 1012 ATGGCACACGTTATCAGATGTGTGATGAAACTGGAGAGCTGGGCCACGTCTCC
 |||||
 1081 ACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGAGGCCATAACCAAGACTTACA
 |||||
 1072 ACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGAGGCCATAACCAAGACTTACA
 |||||
 1141 CCTTCTGCACCCATCCAAATCTCATCGTTGAGCCCGTGCAGCGCGCAGGGAAATTGAA
 |||||
 1132 CCTTCTGCACCCATCCAAATCTCATCGTTGAGCCCGTGCAGCGCGCAGGGAAATTGAA
 |||||
 1201 AACCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTGACGGCGTTGGCTGCTAT
 |||||
 1192 AACCGCGCGTCATGAGTCCAAAAACCTGACGCCGTTCTGACGGCGTTGGCTGCTAT
 |||||
 1261 TGGGTACAGCCCGTGCAGCGGGTACCGCAGAAGAATGTTGCGAATTCAAAACGTCA
 |||||
 1252 TGGGTACAGCCCGTGCAGCGGGTACCGCAGAAGAATGTTGCGAATTCAAAACGTCA
 |||||
 1321 ACCACCCGCCGGAACGCTGTTACGATTCAAAATGTGCAATCGCTTCACCGTGC
 |||||
 1312 ACCACCCGCCGGAACGCTGTTACGATTCAAAATGTGCAATCGCTTCACCGTGC
 |||||
 1381 TATTTTCATGATTGTCGCGTTCTGTTGCGTCTGGATTGCTCTCGACGTTCTGAT
 |||||
 1372 TATTTTCATGATTGTCGCGTTCTGTTGCGTCTGGATCTGCTCTCGACGTTCTGAT

1441 AGCCATGTTCCATCGACGATCCTCGGAATGCCAGAGTAGATTTCATGAATCCACAGGC
 |||||||
 1432 AGCCATGTTCCATCGACGATCCTCGGAATGCCAGAGTAGATTTCATGAATCCACAGGC
 |||||||
 1501 TGC GG TG TCC CGG AC GG CG AAG T CT G CT AC AGT CCC GAG AAA AC GG CT GAG ATT CG C GGG A
 |||||||
 1492 TGC GG TG TCC CGG AC GG CG AAG T CT G CT AC AGT CCC GAG AAA AC GG CT GAG ATT CG C GGG A
 |||||||
 1561 TCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT
 |||||||
 1552 TCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT
 |||||||
 1621 GCAACTACAATCCGTAAGTCTCTCCTCGAGGGCCTACAGCCTATGGGAAAGTAAGACA
 |||||||
 1612 GCAACTACAATCC.....
 1681 GAGGGACAAAACATCATTAAAAAAAAGTCTAATTACGTTTGTACCCCCCTTCCCC
 1625,
 1741 TCCGTGTTGAGGTATACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAACGA
 |||||||
 1625 GTTATACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAACGA
 1801 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTCCCTATCGATGGATCAACCTGGA
 |||||||
 1673 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCGCGTCCCTATCGATGGATCAACCTGGA
 |||||||
 1861 ATACGACAAGATAACCGGATCGTGGGCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
 |||||||
 1733 ATACGACAAGATAAGCCGGATCGTGGGCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
 |||||||
 1921 CAAACGGCTGGATGTGTGCCCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA
 |||||||
 1793 CAAACGGCTGGATGTGTGCCCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA

Translation of SEQKlon95-8.txt: HCK-2 (pUL131x1)

1	ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTGTCTGTGCGCCGTGGTCTGGGTCAAGTGC
1	M R L C R V W L S V C L C A V V L G Q C
61	CAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21	Q R E T A E K N D Y Y R V P H Y W D A C
121	TCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG
41	S R A L P D Q T R Y K Y V E Q L V D L T
181	TTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTGACGTGCTCAAGAGGTGA
61	L N Y H Y D A S H G L D N F D V L K R *

Figure 11

Comparison RACE clone 95-11-FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977

Lower line: SEQKlon95-11.txt, from 1 to 1620

SEQFIX UL131-128.txt:SEQKlon95-11.txt identity= 99.57%(1611/1618)
gap=18.24%(361/1979)

1 GTCTGCAACATGCGGCTGTGTCGGGTGGCTGTTGCTGTGCCCGTGGTCTG
1, ATGCGGCTGTGTCGGGTGGCTGTTGCTGTGCCCGTGGTCTG
61 GGTCAAGTGCCAGCGGGAGACCGCAG...AAAAAAACGATTATTACCGAGTACCGCATTACT
52 GGTCAAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACT
119 GGGACGCGTGCCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCG
112 GGGACGCGTGCCTCGCGCGCTGCCTGACCAAACCGTTACAAGTATGTGGAACAGCTCG
179 TGGACCTCACGTTGAACTACCAACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGC
172 TGGACCTCACGTTGAACTACCAACTACGATGCGAGCCACGGCTTGGACAACTTGACGTGC
239 TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
232 TCAAGAG.....
299 AACGGTAGGTAACCGCATGGGTGTGAAATGACGTTCGAACCTGTGCTTGAGAATCA
237 AATCA
359 ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTACGTCAGAACCGTCGCCGGCA
244 ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTACGTCAGAACCGTCGCCGGCA
419 CCAACAAAAGGACCACGTTAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGAGCCTCG
304 CCAACAAAAGGACCACGTTAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGAGCCTCG
479 AGTTCAGCGTGCAGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCT
364 AGTTCAGCGTGCAGCTTTGCCAACTAGCCTGCGTCACGGAAATAATATGCTACGGCT
539 TCTGCTTCGTACCAACTTCACTGCCCTGCTCTGTGCGCGGTTGGGAAACGCCCTGTCT

424 TCTGCTCGTCACCACCTTCACTGCCTGCTCTGTGCGCGTTGGCAACGCCCTGTCT
 599 GCGTCTCCGTGGTCACGCTAACGGGAACCAAGAATCCGCCCCGCCATGGTCTAAACT
 484 GCGTCTCCGTGGTCACGCTAACGGGAACCAAGAATCCGCCCCGCCATGGTCTAAACT
 659 GACGTATCCAAACCGCATGACGCCGACGTTTACTGTCCCTTTCTCTATCCCTGCC
 544 GACGTATCCAAACCGCATGACGCCGACGTTTACTGTCCCTTTCTCTATCCCTGCC
 719 CCCACGGTCCCCCTCGCAATTCCGGGTTCCAGCGGGTATCAACGGTCCGAGTTCG
 604 CCCACGGTCCCCCTCGCAATTCCGGGTTCCAGCGGGTATTAACGGTCCGAGTTCG
 779 CAACGAGACCCCTGTATCTGCTGTACAACCGGAAAGGCCAGAACCTGGTGGAGAGAACGTC
 664 CAACGAGACCCCTGTATCTGCTGTACAACCGGAAAGGCCAGACCTGGTGGAGAGAACGTC
 839 CACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGAATCAGACCATCCTCCAACG
 724 CACCTGGGTGAAAAAGGTGATCTGGCATCTGAGCGGTCGAATCAGACCATCCTCCAACG
 899 GATGCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGC
 784 GATGCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAAGACGC
 959 CAAGATTTTGAGCGCACATGGTGCCTAACAGCAGACCAAGCTGCTACGTTCGTCGCAA
 844 CAAGATTTTGAGCGCACATGGTGCCTAACAGCAGACCAAGCTGCTACGTTCGTCGCCAA
 1019 CGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGCCCACGTCTTCCG
 904 CGATGGCACACGTTATTAGATGTGTGTGATGAAACTGGAGAGCTGGCCCACGTCTTCCG
 1079 GGACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGAGGCCATAACCAGACTTA
 964 GGACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGAGGCCATAACCAGACTTA
 1139 CACCTCTGCACCCATCCAACTCATCGTTGAGCCGTCGCGCGCAGGGAAATTGG
 1024 CACCTCTGCACCCATCCAACTCATCGTTGAGCCGTCGCGCGCAGGGAAATTGG
 1199 AAAACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGGCTGCT
 1084 AAAACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGGCTGCT
 1259 ATTGGGTACAGCCCGTGCCTGGTACCGCGAGAAGAATGTTGCGAATTCAAAACGT
 1144 ATTGGGTACAGCCCGTGCCTGGTACCGCGAGAAGAATGTTGCGAATTCAAAACGT
 1319 CAACCACCCGCCGGAACGCTGTACGATTCAAAATGTGCAATCGCTCACCGTCGCGTA
 1204 CAACCACCCGCCGGAACGCTGTACGATTCAAAATGTGCAATCGCTCACCGTCG..
 1379 CGTATTTCATGATTGTCTGCGTTCTGTGGTGCCTGGATTGTCTCTGACGTTCTG

1262

1439 ATAGCCATGTTCCATCGACGATCCTCGGGATGCCAGAGTAGATTTCATGAATCCACAG

1262

1499 GCTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCCGG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1262 ACTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCCGG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1559 GATCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1321 GATCGTCACCACCATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1619 CTGCAACTACAATCCGTAAGTCTCTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGA
||||||| |||||

1381 CTGCAACTACAATCT

1679 CAGAGGGACAAACATCATTAAAAAAAAGTCTAATTACGTTTGACCCCCCTTCC

1396

1739 CCTCCGTGTTAGGTTATACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAAC
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1396 GTTATACCTCGAACGCTGACGGCGAATACGCTGCGGCAAAGTGAAC
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1799 GACAAGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1442 GACAAGGCGCAGTACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1859 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1502 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1919 CACAAACGGCTGGATGTGTGCCCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1562 TACAAACGGCTGGATGTGTGCCCGCTAAAATGGCTATATGCTGCAGTGAATAATAAA
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Figure 12**Comparison SEQ 128 B - FIX genomic sequence**

Upper line: FIX genomic sequence

Lower line: SEQ 128 B

5998	ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTACAGC
1	ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTACAGC
6058	CGCGTGCCGCGGGTACGCGCAGAAGAACGTTGCGAATTCTAAACGTCAACCACCCGCCG
61	CGCGTGCCGCGGGTACGCGCAGAAGAACGTTGCGAATTCTAAACGTCAACCACCCGCCG
6118	GAACGCTGTTACGATTCAAAATGTGCAATCGCTTACCGTCGCGTACGTATTTCATGA
121	GAACGCTGTTACGATTCAAAATGTGCAATCGCTTACCGTCGCGTACGTATTTCATGA
6178	TTGTCTGCGTTCTGTGGTGCCTGGATCTGCTCTCGACGTTCTGATAGCCATGTTCC
181	TTGTCTGCGTTCTGTGGTGCCTGGATCTGCTCTCGACGTTCTGATAGCCATGTTCC
6238	ATCGACGATCCTCGGGAAATGCCAGAGTAGATTTCATGAATCCACAGGCTGCGGTGTC
241	ATCGACGATCCTCGGGAAATGCCAGAGTAGATTTCATGAATCCACAGGCTGCGGTGTC
6298	GACGGCGAAGTCTGCTACAGTCAGGAGAAAACGGCTGAGATTGCGGGATCGTACCCACC
301	GACGGCGAAGTCTGCTACAGTCAGGAGAAAACGGCTGAGATTGCGGGATCGTACCCACC
6358	ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
361	ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
6418	CCGTAAGTCTCTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAAA
421	CC.....
6478	CATCATTAAAAAAAGTCTAATTACGTTTGATCCCCCTCCGTGTTGA
423

Translation of SEQ128 B x 1.txt: HCK-3 (pUL128x1)

1 ATGAGTCCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTACAGC
1 M S P K N L T P F L T A L W L L L G H S

61 CGCGTGCCGGGTACCGCGAGAAGAATGTTGCGAATTCACTAAACGTCACCACCCGCCG
21 R V P R V R A E E C C E F I N V N H P P

121 GAACGCTGTTACGATTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTCATGA
41 E R C Y D F K M C N R F T V A Y V F S *

Figure 13

Comparison SEQ 128 A - FIX genomic sequence**Upper line: FIX-BAC****Lower line: SEQ128 A**

5998	ATGAGTCCCAAAACCTGACGCCGTCTTGACGGCGTTGGCTGCTATTGGGTACAGC
1	ATGAGTCCCAAAACCTGACGCCGTCTTGACGGCGTTGGCTGCTATTGGGTACAGC
6058	CGCGTGC CGCGGGTACGCGCAGAAGAATGTTGCGAATTCAAAACGTCAACCACCCGCCG
61	CGCGTGC CGCGGGTACGCGCAGAAGAATGTTGCGAATTCAAAACGTCAACCACCCGCCG
6118	GAACGCTGTTACGATTCAAAATGTCAATCGCTTACCGTCGCGTACGTATTTTATGA
121	GAACGCTGTTACGATTCAAAATGTCAATCGCTTACCGTCGCGTACGTATTTTATGA
6178	TTGTCTGC GTTCTGTGGTGC GTCTGGATTGTCTCTCGACGTTCTGATAGCCATGTTCC
166
6238	ATCGACGATCCTCGGGAAATGCCAGAGTAGATTTCATGAATCCACAGGCTGC GG TGCCG
166 GCTGC GG TGCCG
6298	GACGGCGAAGTCTGCTACAGTCCCAGAAAACGGCTGAGATTGCGGGATCGTCACCACC
178	GACGGCGAAGTCTGCTACAGTCCCAGAAAACGGCTGAGATTGCGGGATCGTCACCACC
6358	ATGACCCATTCA TTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
238	ATGACCCATTCA TTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
6418	CCGTAAGTCTCTCCCTCGAGGGCCTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
298	CC.....
6478	CATCATTA AAAAAGTCTA ATTTCACGTTTGTACCCCCCTCCCGTGTGTA
300
6538	GGTTATACTCGAAGCTGACGGCGAATACGCTGCGCAAAGTGAACGACAAGGCGCAGT
300	.GTTATACTCGAAGCTGACGGCGAATACGCTGCGCAAAGTGAACGACAAGGCGCAGT
6598	ACCTGCTGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA

359 ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
6658 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
419 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
6718 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCC
479 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGT

Translation of SEQ128 A: HCK-4 (pUL128)

1 ATGAGTCCCCAAAACCTGACGCCGTCTGACGGCGTTGTGGCTGCATTGGGTACAGC
1 M S P K N L T P F L T A L W L L L G H S

61 CGCGTGCCGCCGGTACGCCAGAAGAATGTTGCGAATTCAAAACGTCACCACCCGCCG
21 R V P R V R A E E C C E F I N V N H P P

121 GAACGCTGTTACGATTCAAAATGTGCAATCGCTTCACCGTCGCACTGCGGTGTCCGGAC
41 E R C Y D F K M C N R F T V A L R C P D

181 GGCGAAGTCTGCTACAGTCCCAGAACGGCTGAGATTGGCGGGATCGTCACCACCATG
61 G E V C Y S P E K T A E I R G I V T T M

241 ACCCATTCAATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAATCTG
81 T H S L T R Q V V H N K L T S C N Y N L

301 TTATACCTCGAACGCTGACGGCGAATACGCTGCGCAAAGTGAACGACAAGGCGCAGTAC
101 L Y L E A D G R I R C G K V N D K A Q Y

361 CTGCTGGGCCGCTGGCAGCGTTCCCTATCGATGGATCACACCTGAAATACGACAAGATA
121 L L G A A G S V P Y R W I N L E Y D K I

421 ACCCGGATCGTGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
141 T R I V G L D Q Y L E S V K K H K R L D

481 GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA
161 V C R A K M G Y M L Q *

Figure 14

Translation of SEQUL130: HCK-5 (pUL130)

1	ATGCTACGGCTCTGCTCGTCACCACCACTTCACTGCCTGCTCTGTGCGCGGTTGGCA
1	M L R L L L R H H F H C L L L C A V W A
61	ACGCCCTGTCTGGCGTCTCCGTGGTTACGCTAACGGGAACCAAGAATCCGTCCCCGCCA
21	T P C L A S P W F T L T A N Q N P S P P
121	TGGTCTAAACTGACGTATCCCAAACCGCATGACGCCGACGTTTACTGTCCCTTTCTC
41	W S K L T Y P K P H D A A T F Y C P F L
181	TATCCCTGCCCGCACGGTCCCCCTCGCAATTCCGGGTTCCAGCGGGTATCAACGGGT
61	Y P S P P R S P S Q F P G F Q R V S T G
241	CCCGAGTGTGCCAACGAGACCGCTGTATCTGCTGTACAACCGGAAGGCCAGACCTGGTG
81	P E C R N E T L Y L L Y N R E G Q T L V
301	GAGAGAAGCTCCACCTGGTGAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACC
101	E R S S T W V K K V I W Y L S G R N Q T
361	ATCCTCCAACGGATGCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGC
121	I L Q R M P R T A S K P S D G N V Q I S
421	GTGGAAGACGCCAAGATTGGAGCGCACATGGTGCCAACGAGACCAAGCTGCTACGT
141	V E D A K I F G A H M V P K Q T K L L R
481	TTCGTCGTCAACGATGGCACACGTTATCAGATGTGTGATGAAACTGGAGAGCTGGGCC
161	F V V N D G T R Y Q M C V M K L E S W A
541	CACGTCTTCCGGACTACAGCGTGTCTTCAGGTGCGATTGACGTTACCGAGGCCAAT
181	H V F R D Y S V S F Q V R L T F T E A N
601	AACCAGACTTACACCTCTGCACCCATCCCAATCTCATCGTTGA
201	N Q T Y T F C T H P N L I V *